

FIGURE 1

GGACTAATCTGTGGGAGCAGTTATTCCAGTATCACCCAGGGTGAGCCACACCAGGACTGT
GTTGAAGGGTGTCCCCCTAAATGTAATACCTCCTCATCTTCTTACACAGTG
TCTGAGAACATTACATTATAGATAAGTAGTACATGGTGGATAACTCTACTTTAGGAGGA
CTACTCTTCTGACAGTCCTAGACTGGTCTTCTACACTAAGACACCATGAAGGAGTATGTG
CTCCTATTATTCTGGCTTGTGCTGCCAACCTTCTTAGCCCTCACACATCGCACT
GAAGAACATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATG
ATGATGATGATGAGGACAACCTCTTTCCAACAAGAGAGCCAAGAAGCCATTTC
TTTGATCTGTTCCAATGTGTCATTGGATGTCAGTGCTATTCAAGGAGTTGATCTG
AGATTTAGGTTGACCTCAGTCCAACCAACATTCCATTGATACTCGAATGCTGATCTC
AAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTAAAGGACTCACTTCACTTATGGT
CTGATCCTGAACACAACAAGCTAACGAAGATTACCCAAAAGCCTTCTAACACAAAGAA
GTTGCGAAGGCTGTATCTGCCCACAATCAACTAAGTGAATACCACTTAATCTCC
CATTAGCAGAACTCAGAATTCAATGAAAATAAGTTAAGAAAATACAAAAGGACACATTCAA
GGAATGAATGCTTACACGTTGGAAATGAGTGCAAACCCCTTGTATAATGGGATAGA
GCCAGGGGCATTGAAGGGGTGACGGTGTCCATATCAGAATTGCGAGAAGC
CAGTTCTAAAGGCTTACCAACTTATTGGAGCTTCACTTAGATTATAATAAAATTCA
ACAGTGGAACTTGAGGATTTAACGATAAAAGAAACTACAAAGGCTGGCCTAGGAAACAA
CAAATCACAGATATCGAAAATGGAGTCTGCTAACATACCACGTGTGAGAGAAATACATT
TGGAAAACAATAAAACTAAAAAAATCCCTCAGGATTACCAAGAGTTGAAATACCTCC
ATCTTCCTTCATTCTAATTCAATTGCAAGAGTGAGTAAATGACTCTGTCCAACAGTG
AAAGATGAAGAAATCTTATACAGTGAATAAGTTATTCAACAAACCCGGTGAAATACTGG
AAATGCAACCTGCAACATTCTGTTGTTTGAGCAGAATGAGTGTCA
GGAATGTAATATTAGTAATTGTAATGTCCATTAAATATAAGATTCAAAATCCCTACATT
TGGAAACTTGAACTCTATTAAATAATGGTAGTATTATATAACAGCAAATATCTATTCTCA
AGTGGTAAGTCCACTGACTTATTGACAAGAAAATTCAACGGAA
GATAACATAAGGGTTGAGAGAAACAAGCATCTATTGCA
CTTACATAATCTCATGCTTGACCATTCTTCTTCATAACAAAAGTAAGATATTGGTA
TTAACACTTGTATCAAGCACATTAAAAGAACTGTACTGTAATGGAATGCTTGACT
TAGCAAAATTGCTCTTCATTGCTTTAGAAAAACAGAATTAAACAAAGACAGTAATGT
GAAGAGTGCATTACACTATTCTTATTCTTAGTAACCTGGTAGTACTGTAATATTTAAT
CATCTTAAAGTATGATTGATATAATCTTATTGAAATTACCTTATCATGCTTAGAGCCGT
CTTATGTTAAAACATAATTCTAAAATAAGCCTTCAGTAAATGTTCA
TAAATGCTACTCATAAGAGCTGGTTGGGCTATAGCATATGCTTTTTTAATTATT
ACCTGATTAAAATCTGTAAAACGTGTAGTGTTCATAAAACTGTA
AATGATCCGCTATTATAAGCTTTAATAGCATGAAAATTGTTAGGCTATATAACATTGCCAC
TTCAACTCTAAGGAATATTTGAGATATCCCTTGGAAAGACCTGCTTGGAAAGAGCCTGGA
CACTAACATTCTACACCAAATTGTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAAACAGACAGAAACCGAAAGCTCTA
TATAAATGCTCAGAGTTCTTATGTATTCTTATTGGCATTCAACATATGTA
ACAGGGAAATTTCATTAAAATATTGGTTGAAAT

FIGURE 2

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392
<subunit 1 of 1, 379 aa, 1 stop
<MW: 43302, pI: 7.30, NX(S/T): 1
MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDEDNSLFPTREPR
SHFFPFDFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNNKLTKIHPKAFLTTKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ
KDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNNKITDIENSLANI PRVREIHLENNKLKKIPSGLPEL
KYLQIIIFLHSNSIARGVVNDFCPTVPKMKSLSAISLFNNPVKYWEMQPATFRCVLSRMSV
QLGNFGM
```

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGCCGCAGCACCAGCCCCGGCCCTCCGCCCTCCGACTCGGCCCTCC
CTCCCTCCGCCGCTCCCGCCTCCCTCCCTCCCTCCCTCCAGCTGTCCCGTTCGCGTCATGCCGAGCCTCCC
GGCCCCGCCGGCCCCGCTGCTGCTCCCTGGCTGCTGCTCGGCTCCGGCCGGCCGCCGGCCAGA
GCCCGGGCTGCTGCCCATCGTTCTGAGAAGGAGCCGCTGCCGTTGGAGCGGCAGGGCTCACCTCGCGG
GAAGGTCTATGCCTTGACGAGACGAGTGGCACCCGGACCTAGGGCAGCCATTGGGTATGCGCTGCGTGTG
CGCCTGCGAGGCCCTCAGTGGGTCGCCGTACCAAGGGGCCCTGGCAGGGTCAGCTGCAAGAACATCAAACAGA
GTGCCCAACCCCGGCCCTGTGGCAGCCAGCTGCCGGACACTGCTGCCAGACCTGCCAGGGCAGGAGCGCAG
CAGTCGGAGCGCAGCCGAGCGGCCCTGTCAGTATCCGGGACCCGGAGCAGTCAGTTAGCGACCG
CGGGGAGCAGGCAGGCGCTGAGGAGCGGGCCCTGGTACGCCACACGGACTTCGTGGCCTGCTGACAGGCCGAG
GTCGCAAGGCCGTGGCACGAGCCGAGTCTGCTGCGCTCTAGCCTCCGCTCTATCTCTACAGGCCGCT
GGACGCCCTTACCAAGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTTGAGCACCCCTGAGCCCCACCCA
AGATGGCCTGGTCTGTTGGGTGAGGGGGCAGTCCTCGGTTGCTCTGCCGCTCCCTAGGGCAGAACAGCTGCA
TGTGGCACTTGTGACACTCACTCACCCCTCAGGGGAGGTCTGGGGCCCTCTCATCCGGCACCGGGCCCTGGCTGC
AGAGACCTTCAGTGCATCCTGACTCTAGAAGGCCCCCACAGCAGGGCTAGGGGCATCACCTGCTACTCT
CAGTACACAGAGGACTCCCTGCTTTGCTGCTCTCCGAGGGCTGTTGAAACCCAGGAGTGGGGACTAAC
CCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGCAGCTACTGCGAGAACCTCAGGCCAATGTCTCAGCCA
GGAACCAGGCTTGCTGAGGTGCTGCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTCTGGGGAGCTGCA
GATGGCCCTGGAGTGGCAGGCAGGGCTGCCATAGGACACATTGCTGCCAGGAAGAGCTGCAGC
CCTGCAAAGTGTCTTGTGGGGCTGATGCCCTGATCCCAGTCCAGACGGGTGCTGCCGGCTCAGCCAGCCTCAC
GCTGCTAGGAAATGGCTCCCTGATCTATCAGGTGCAAGTGGTAGGGACAAGCAGTGAGGTGGTGCCATGACACT
GGAGACCAAGCCTCAGCGGAGGGATCAGCGCACTGTCCTGTGCCACATGGCTGGACTCCAGGCCAGGAGCACAC
GCCGTGGGTATCTGCCCTGGGTGCCGAGGGCTCATATGCTGCTGAGAACATGAGCTCTCCTGAACGT
GGGCACCAAGGACTTCCAGCGGAGAGCTCGGGGACGTGGCTGCCCTGCCCTACTGTGGGATAGGCCAGCCTCG
CCATGACACGCTGCCGTGCCCTAGCAGGAGCCCTGGTCTACCCCTGTGAAGAGCCAAGCAGCAGGGCACGC
CTGGCTTCCCTGGATACCCACTGTCACCTGCACTATGAAGTGTGCTGGCTGGCTGGTGGCTCAGAACAGG
CACTGTCACTGCCAACCTCCCTGGCCTCTGGAACGCCAGGGCCTCGGGCTGCTGAAGGGATTCTATGGCTC
AGAGGCCAGGGTGGTGAAGGACCTGGAGCGGAAGTGTGCGGCACCTGGCAAAGGCATGGCTCCCTGAT
GATCACCAACCAAGGGTAGCCCCAGAGGGGAGCTCGAGGGCAGGTGACATAGCCAACCAATGTGAGGTGGCG
ACTGCGCTGGAGGGCCGGGGCGAGGGGGTGGGGCTCCGGATACAGCCTCTGCTGCCGCC
TGTGGTGCCTGGTCTCCGGCCCTAGGCCCGCAAACCTGGTGGTCTGGGGGCCGGAGACCCAAACACATG
CTTCTCGAGGGCAGCAGGCCAACGGGCTCGCTGGGCCAACTACGACCCGCTCTGCTCACTGAC
CTGCCAGAGACGAACGGTGTACTGTGACCCGGTGGTGTGCCAACGCCAGCTGCCAACACCCGGTGCAGGCTCC
CGACCAGTGTGCCCTGTTGCCCTGAGAAACAAGATGTCAGAGACTTGCCAGGGCTGCCAGGAGGCCGGACCC
AGGAGAGGGCTGCTATTGATGGTACCGGAGCTGGGGCAGCGGGTACGCGTGGCACCCGTTGTGCC
CTTGGCTTAATTAAAGTGTGCTGCAACCTGCAAGGGGGACTGGAGAGGTGCACTGTGAGAACGGCAGTG
TCCCCGGCTGGCCTGTGCCAACGCCCTGTGCTGTCACCCACCGACTGCTGCAAACAGTGTCCAGTGGGGCTGG
GGCCCAACCCCAAGCTGGGGACCCATGCAAGGCTGATGGGCCCGGGCTGCCGTTTGCTGGCAGTGGTCCC
AGAGAGTCAGAGCTGGCACCCCTCAGTGCCCTTTGGAGAGATGAGCTGTATCACCTGCAAGATGTGGGGCAGG
GGTGCCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCTGTGGCTGGGGAGGGAGAGTCGATGCTGTT
CCGCTGCAGGCCAACGGCGGGCCCCAGAGACCAGAACGAGTCAGGAGCTGGAGAAAAGAACGCCAGGGCTT
GCATTCTCTGTGGGAAGGCCAGTGCCTTGTCCCTGTGCTGCTACTCCCACCCACTACCTCTGGGAA
CCACAGCTCCACAAGGGGGAGAGGCAGCTGGGCCAGACCGAGGTGACAGCCACTCCAAGTCTGCCCTGCCACCC
TCGGCCTCTGTCCGTGAAGCCCCACCCCTTCTCTGTACATAATGTCAGTGGTTGGATTAAATT
TCTTCACTCAGCACCAAGGGCCCCGACACTCCACTCCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAG
TTTGTATTATTAAAACATTCTTTCAAGTCAAAAAAAAAAAAAA

FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, PI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLGLLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRAAGCTFGGVYALDE
TWHPDLGQPGVMRCVLCACEAPQWGRTRGPGRVSKNIKPECPTPACGQPRQLPGHCCQT
CPQERSSSERQPSGLSFEYPRDPEHRSYSDRGEPGAERARGDHTDFVALLTGPRSQAVER
ARVSSLRSSLRFSISYRRLDPRTRIRFSDNSGVLFEHPAAPTQDGLVCGVWRRAVPRLSLRL
LRAEQLHVALVTLTHPSGEVGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTLSDTED
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQQLLRELQANVSAQEPGFAEVLPNLTQEMD
WLVLGELQMALEWAGRPGLRISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN
GSЛИYQVQVVGTSSEVVAMTLETKPQRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML
LQNELFLNVGTKDFPDGELRGHVAALPYCGHSARHDTPVLAGALVLPPVKSQAAGHAWLS
LDTHCHLHYEVLLAGLGGSEQGTVTAHLLGPPGTPGPRRLKGFYGSEAQGVVKDLEPELLR
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGLRLEAAGAEGVRALGAPDTASAAPPVV
PGLPALAPAKPGGPGRPRDPNTCFEGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVCP
PPSCPHVQAPDQCCPVCPEKQDVRLPGLPRS RD PGEGCYFDGDRSWRAAGTRWHPVVPPF
GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPVRVNPTDCCKQCPVSGAHPQLGDPMQADG
PRGCRFAGQWFPEQSWSHPSVPPFGEMSCITCRCGAGVPHCERDDCSLPLSCGSGKESRCCS
RCTAHRRPPETRTDPELEKEAEGS

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

FIGURE 5

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTGCAGCTCTCGCAGCTGCCACTGCCACCGCCGCCGTCACTGCG
TCCTGGCTCCGGCTCCCGCCCTCCCGGGCGGCCATGCAAGCCCCGCCGCCAGGCAGCCCAGGGTGCAGCTGC
TGCCCGCGCTGGCCCTGCTGCTGCTGCTCGGAGGGGGCCCGAGGCAGCTCCCTGGCAACCGGTGCCCG
CCCGGCCCTTGTCTGCGCCGGCGTGCAGCCCTGCCGAATGGGGGTGTGACCTCGCGCCCTG
AGCCGGACCGCAGCACCCGGCCCCGCCGGCAGCCTGGCTACAGCTGCACCTGCCCGCCGGATCTCCGGCG
CCAAGTGCAGCTTGTGCAGATCCTGTGCAGCAACCCTGTGACCATGGCAACTGCAGCAGCAGCAGCA
GCAGCAGCGATGGCTACCTCTGCATTGCAATGAAGGCTATGAAGGTCCAAGTGTGAAACAGGCACCTCCAGTC
TCCCAGCCACTGGCTGGACGAATCCATGGCACCCCGACAGCTTCAGGCTGTTCTGCTACTCAGGAGCCTGACA
AAATCCTGCCTCGCTCAGGCAACGGTACACTGCTCACCTGGCAGCCAAAACAGGGCAGAAAGTTGTAGAAA
TGAAATGGGATCAAGTGGAGGTATCCAGATATTGCCTGTGGAATGCCAGTTCTAACAGCTCTGCCGGTGGCC
GCCTGGTATCCTTGAAGTGCACAGAACACCTCAGTCAAGATTGCCAGATGCCACTGCCACTGATTTC
TCTGGAAGGTACGGCCACAGGATTCAAACAGTGCCTCCCTCATAGATGGACGAAGTGTGACCCCCCTCAGGCTT
CAGGGGACTGGTCTCCTGGAGGGAGATGCTCGCCTGGGAATAATCACTTATTGGTTTGTGAATGATTCTG
TGACTAAGTCTATTGTGGCTTGCCTTAACCTCTGGTGTGAAGGTACGGTACGACACTGTGTCGCCGGGGAGAGTCACG
CAAATGACTTGGAGTGTTCAGGAAAAGGAAATGCACACAGAACCGTCAGAGGAACCTTTCTGTACCTGTG
AGGAGCAGTACGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAAACAACGCGAGCT
GTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTCACCTGTGTTGCCCTGGTTACTGGAGAGCTT
GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCAATTCCAGTCTCAGTGGAT
TCACCTGCCAGTGTCCAGAAGGATACTTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCCCTCGTCTCCGT
GCCAGAACACGGCACCTGCTATGTGGACGGGGTACACTTACCTGCAACTGCAGCCGGGCTTCACAGGGCGA
CCTGTGCCAGCTTATTGACTTCTGTGCCCTCAGCCCTGTGCTCATGGCACGTGCCGAGCGTGGGACCCAGCT
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ACTGTGAATTGTACAAGGATCCCTCGCTAACGTCACTGTGACAGGAGCCACCTGTGACAGCGACGGCTGA
ATGGCACGTGCATCTGTGACCCGGTTACAGGTGAAGAGTGCACATTGACATAATGAATGTGACAGTAACC
CCTGCCACCATGGTGGAGCTGCCCTGGACCAGCCAAATGGTTATAACTGCCACTGCCGCATGGTGGGAG
CAAACGTGAGATCCACCTCCAATGGAAGTCCGGGACATGGGGAGAGCCTACCAACATGCCACGGACTCCC
TCTACATCATCATTGGAGCCCTCTGCGTGGCTTCATCCTTATGCTGATCATCCTGATCGTGGGATTGCCGCA
TCAGCCGATTGAATACCAGGGTTCTCAGGCCAGCCTATGAGGAGTTCTACAACGTGCCGACATCGACAGCG
AGTTCAGCAATGCCATTGCATCCATCGGCATGCCAGGTTGAAAGAAATCCCGGCTGCAATGTATGATGTGA
GCCCATGCCCTATGAAGATTACAGTCCCTGATGACAAACCTGGTCACACTGATTAAGAAACTAAAGATTGTAAT
CTTTTTGGATTATTTCAAAAGATGAGATACTACACTCATTTAAATATTTAAGAAAATAAAAGCTTAA
GAAATTAAAATGCTAGCTGCTCAAGAGTTTCAGTAGAATATTAAGAAACTAATTTCTGAGCTTTAGTTG
GAAAAAATATTTAAAACAAATTGTGAAACCTATAGACGATTTAATGTACCTCAGCTCTAAACTGT
GTGCTTCTACTAGTGTGCTCTTCACTGTAGACACTATCAGAGACCCAGATTAATTCCTGTGGTTTGTACA
GAATAAGTCTAATCAAGGAGAAGTTCTGTTGACGTTGAGTGCCGGCTTCTGAGTAGAGTTAGAAAACCAC
GTAACGTAGCATATGATGTATAATAGAGTATACCCGTTACTTAAAAGAAGTCTGAAATGTCGTTTGTGGAAA
AGAAAATAGTTAAATTACTATCCTAACCGAATGAAATTAGCCTTGCCTTATTCTGTGCATGGTAAGTAAC
TTATTCTGCACTGTTGTAACCTTGTGGAAACATTCTTCGAGTTGTTGTCATTTCTGTAACAGTCG
TCGAACTAGGCCTCAAAACATACGTAACGAAAAGCCTAGCGAGGCAAATTCTGATTGATTTGAATCTATATT
TTCCTTAAAAGTCAAGGGTTCTATATTGTGAGTAATTAAATTACATTGAGTTGTTGCTAAGAGGTAG
TAAATGTAAGAGAGTACTGGTCTTCAGTAGTGTGAGTATTCTCATAGTGCAGCTTATTATCTCCAGGATGTT
TTTGTGGCTGTATTGATTGATATGTGCTTCTGATTCTGCTAATTCCAACCATATTGAATAATGTGATC
AAGTCA

TOP SECRET - 08300

FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR
PEPDHQHPPAPAGEPGYSCTCPAGISGANCQLVADPCASNPCHHGNSSSSSDGYLCICN
EGYEGPNEQALPSLPATGWTESMAPRQLQPVPATQEFDKILPRSQATVTLPTWQPKTGQKV
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQ
QCSLIDGRSVTPLQASGLVLLEEMALGNNHFIGFVNDSVTKSIVALRLTLLVVKVSTCVPG
ESHANDLECSKGKCTKPSEATFSCTCEEQYVGTCEEYDACQRKPCQNNASCIDANEKQD
GSNFTCVCLPGYTGELCQSKIDYCILDPCRNGATCISSLSGFTCQCPEGYFGSACEEKVDPC
ASSPCQNNGTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSYKCLCDPG
YHGLYCEEYNECLSAPCLNAATCRDLVNGYECVCLAELYKGTHCELYKDPCANVSCNGATC
DSDGLNGTCICAPGFTGECDIDINECDSNPCHGGSCLDPNGYNCHCPHWVGANCEIHL
QWKSGHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYN
CRSIDSEFSNAIASIRHARGKKSRPAMYDVSPIAYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

FIGURE 7

CTCTGGAAGGTACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTCAGGCTTCAGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTGGGAATA
ATCACTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCGCTTAAC
CTGGTGGTGAAGGTACGCACCTGTGTGCCGGGGAGAGTCACGCAAATGACTGGAGTGTTC
AGGAAAAGGAAAATGCACCAACGAAGCCGTAGAGGAACTTTCTGTACCTGTGAGGAGC
AGTACGTGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAACAAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTCACCTGTGTTGCCTTCC
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

FIGURE 8

CTCTGGAAGGTACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTCAGGCTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTGGGAATA
ATCACTTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCCTTAACCT
CTGGTGGTGAAGGTACGCACCTGTGTGCCGGGGAGAGTCACGCAAATGACTGGAGTGTTC
AGGAAAAGGAAAATGCACCACGAAGCCGTCAAGAGGCAACTTTCTGTACCTGTGAGGAGC
AGTACGTGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAACAAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGAGCAATTCACCTGTGTTGCCTTCC
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

DIE SIEBEN EIL. u. DIE ZEIT

FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCCAGCCTGTAACCTGTGCCTACACCACGCCAG
GCCCCCCCAGAGCCCTCACCAACGCTGGCGCCCCAGAGCCCACACCATGCCGGCACCTAC
GCTCCCTGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGCCCT
GATGCGGGACTTCCGCTCGTGGACGGCCACAACGACCTGCCCCTGGTCCTAAGGCAGGTT
ACCAGAAAAGGGCTACAGGATGTTAACCTGCGCAATTTCAGCTACGCCAGACCAGCCTGGAC
AGGCTTAGAGATGCCCTCGTGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGGATGCCCTGCGCCTACCCCTGGAGCAGATTGACCTCATACGCCATGTGCGCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCCTCATCGGTGTAGAGGGTGCCACTCGCTGGACAATAGCCTCTCCATTTACGTACCTT
CTACATGCTGGAGTGCCTACCTGACGCTACCCACACCTGCAACACACCCCTGGCAGAGA
GCTCCGCTAAGGGCGTCCACTCCTCTACAACACATCAGCGGGCTGACTGACTTTGGTGAG
AAGGTGGTGGCAGAAATGAACCGCCTGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
TGTGGCACGGCGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCACTCGCTGCC
GGGGTGTGTGCAACAGTGCCTCGGAATGTTCTGATGACATCCTGCAGCTCTGAAGAAGAAC
GGTGGCGTGTGATGGTGTCTTGTCCATGGGAGTAATAACAGTGCACCCATCAGCCAATGT
GTCCACTGTGGCAGATCACTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGA
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CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCC
TCGTGGAAACCTGCTGCGGTCTTCAGACAAGTGGAAAGGTACAGGAAGAAAACAAATGGC
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TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACACTGAGATTCCCATA
CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAG
TCCTTGCAGTTGTGGCACCTTCCAGTCCTTATTCTGTGGCTTGATGACCCAGTTAGTCC
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCCTGTTGTGCAGGCACA
AATATTCTGAAATAATGTTGGACATAG

FIGURE 10

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595
<subunit 1 of 1, 433 aa, 1 stop
<MW: 47787, pI: 6.11, NX(S/T): 5
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QTSLDRLRDGLVGAQFW SAYVPCQTQDRDALRLTLEQIDLIRRMCA SYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLCNTPWAESSAKGVHSFYNNISGL
TDFGEKVV AEMNRLGMMV DLSHVSDA VARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVMV SLSMGVIQCNP SANVSTVADHFDHI KAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPV LIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEE KWQS PLEDKFPDEQLSSS
CHSDL SRLRQR QSLTSGQ ELTEIPIHWTAKLPAKWSVSESSPHMAPV LAVVATFPV LILWL
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N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

FIGURE 11

AAAACCTATAATATTCCGGATTATTCAACCGTCCCACCATCGGGCGGATCCGCGGCCG
CGAATTCTAAACCAACATGCCGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA
CCCAGGGCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCCGCTCGTGGACGGCCAC
AACGACCTGCCCTGGTCCAAGGCAGGTTACCAGAAAGGGCTACAGGATGTTAACCTGCG
CAATTCAGCTACGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGCGCCAGT
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTACCCCTGGAG
CAGATTGACCTCATGCCGATGTGCTCCTATTCTGAGCTGGAGCTGTGACCTCGC
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGCCACTCGC
TGGACAATAGCCTCTCCATCTTACGTACCTCTACATGCTGGAGTGCCTACCTGACGCTC
ACCCACACCTGCAACACACCCCTGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTCTACAA
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGCA
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG
GCACCTGTGATCTTCTCCACTCGGCTGCCGGGGTGTGCAACAGTGCTCGGAATGTTCC
TGATGACATCCTGCAGCTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTGTCCATGG
GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTCGACCACATC
AAGGCTGTCATTGGATCCAAGTTCATCGGATTGGTGGAGATTATGATGGGGCGGCAAATT
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GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTCGTGGAAACCTGCTGCGGTCTCAGACAA
GTGGAAAAGGTACAGGAAGAAAACAAATGCAAAGCCCCTGGGAGGACAAGTCCCGATGA
GCAGCTGAGCAGTTCTGCCACTCCGACCTCTCACGTCTCGTCAGAGACAGAGTCTGACTT
CAGGCCAGGAACACTGAGATTCCCATACACTGGACAGCCAAGTTACCAGCCAAGTGGTCA
GTCTCAGAGTCCTCCCCCACCCTGACAAAACTCACACATGCCACCCTGCCCCAGCACCTGA
ACTCCTGGGGGACCGTCAGTCTTCCCTTCCCCAAAACCCAAGGACACC

FIGURE 12

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX(S/T): 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFW SAYVPCQTQDRDALRLTLEQIDLIRRMCA SYSELELVTSAKALND
TQKLA CLIGVEGGHSLDN SLSILRTFYMLGVRYLT LHTCNT PWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMV DLSHVSDA VARRA LEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGG VVMVSLSMGV I QCNPSANV STVADHFDHI KAVIGSKFIGI GGDYDGAGKF PQGLE
DVSTYPV LIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEEENKWQS PLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHDKTHTC PPPCPAPELLGGP
SVFLFPPPKPKDT
```

FIGURE 13

CGCCCAGCGACGTGCGGGCGGCCTGGCCCCGCGCCCTCCCGCGCCCGGCCCTGCGTCCC CGGCC
CTGCGCCACCGCCGCCGAGCGCAGCGCAGCCCGCCGCGCGCCCCCGCAGCGCCGGCCCCATGCCC
GCCGGCCGCCGGGGCCCCGCCCAATCCGCGGCCGGCCGCCGCGTTGCTGCCCTGCT
GCTGCTGCTCTGCGTCCTCGGGGCCGCGAGCCGGATCAGGAGCCCACACAGCTGTGATCA
GTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCACCTGCTCAGTGCACGGA
GACCCACCAGGAGCCACCGCCGAGGGCCTACTGGACCCCTAACGGCGCCGCTGCC
TGAGCTCTCCGTGTACTAACGCCTCCACCTTGGCTCTGGCCCTGGCCAACCTCAATGGT
CCAGGCAGCGGTGGGGACAACCTCGTGTGCCACGCCGTGACGGCAGCATTGGCTGGC
TCCTGCCTCTATGTTGGCCTGCCAGAGAAACCGTCAACATCAGCTGCTGGTCCAAGAA
CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCACGGGAGACCTTCCACACCA
ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGCCAGGACAACACATGTGAGGAGTAC
ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGAT
CTGGGTGGAGGCCACCAACCGCCTGGCTCTGCCCGCTCCGATGTACTCACGCTGGATATCC
TGGATGTGGTGACCACGGACCCCCCGCCGACGTGACGTGAGGCCGTCGGGGCCTGGAG
GACCAGCTGAGCGTGCCTGGGTGTCGCCACCCGCCCTAACGGATTCCTCTTCAAGCAA
ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGACGATGTGAGCA
ACCAGACCTCCTGCCGCTGGCCGGCCTGAAACCCGGCACCGTGTACTCGTCAAGTGC
TGCAACCCCTTGGCATCTATGGCTCCAAGAAAGCCGGATCTGGAGTGAGTGGAGCCACCC
CACAGCCGCTCCACTCCCCGCACTGAGGCCGGGCCGGCGGGCGTGCACCGC
GGGGCGGAGAGCCGAGCTCGGGCCGGTGCAGCGAGCTAACGAGTCCCTGGCTGGCTC
AAGAAGCACCGTACTGCTCCAACCTCAGCTCCGCCCTACGACCAGTGGCGAGCCTGGAT
GCAGAAGTCGACAAGACCCGCAACCAGGACGAGGGATCCTGCCCTGGCAGACGGGCA
CGGCGAGAGGTCCAGATAAGCTGTAGGGCTCAGGCCACCCCTGCCACGTGGAGA
CGCAGAGGCCAACCAAACGGCCACCTCTGTAACCTCACTCAGGCCACCTGAGCCAC
CCTCAGCAGGAGCTGGGTGGCCCTGAGCTCAACGCCATAACAGCTCTGACTCCACGT
GAGGCCACCTTGGGTGCAACCCAGTGGGTGTGTGTGAGGGTTGGTTGAGTTGC
CTAGAACCCCTGCCAGGGCTGGGGTGAAGAAGGGAGTCATTACTCCCCATTACCTAGGGCC
CCTCCAAAAGAGTCCTTAAATAAATGAGCTATTAGGTGCTGTGATTGTGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAACAAAAAAA

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FIGURE 14

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pi: 9.42, NX(S/T): 6

MPAGRRGPAAQSARRPPPLPLLLLCLVLAGPAGSGAHTAVISPQDPPTLLIGSSLLATCSV
HGDPPGATAEGLYWTLNRRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTGAHGETFLHTNYSKYKLRWYGQDNTCEE
YHTVGPHSCHIPKDLALFTPYEIWVEATNRGSAESDVLTLDILDVVTTDPPPVDHVSRVGG
LEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDKVVDDVSNQTSCRLAGLKPGTVYFVQ
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSGPVRRELKQFLG
WLKKHAYCSNLSFRPLYDQWRAWMQKSHKTRNQDEGILPSGRGTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

FIGURE 15

CCCCACCGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAAACGCTCGCAGCCACAAAGGGATGAAATTCTTCTGGACATCCTC
CTGCTTCTCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA
GAGGAGAAAATCAGTCACCGGCAGAACATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GAUTGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTG
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA
GGCATTCTCCTGCAATGACGAAGAATAACCATGGCCATATTGTCAGTGTGGCTCGGCAG
CTGGACATGTCTCGTCCCCTCTTACTGGCTACTGTTCAAGCAAGTTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACTGGCTGCCTACAAATACTGGAGTCAAAACACATG
TCTGTGTCCTAATTGTAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTTCTATAGCTTTTAACAACATTGGAAAGGATCCTCCTGAGCGTT
CCTGGCAGTTTAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAAGCACCTAGTTCTGAAAATGATTACCAAGGTTAGGTGATGTCATCTA
ATAGGCCAGAATTAAATGTTGAACCTCTGTTCTAATTATCCCCATTCTCAATA
TCATTTGAGGCTTGGCAGTCTCATTACTACCACCTGTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTAAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGTTGCAA
AATTGTACCATAACGTTATTAAACATATATTATTATTGATTGACTTAAATTGTTG
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTCTAAATAAAA
TGAAGGACTATCTAGTGGTATTTCACAATGAATATCATGAACCTCAATGGTAGGTT
ATCCTACCCATTGCCACTCTGTTCTGAGAGACCTCACATTCAATGCCAACATTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGATTAAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
AAAAAAA
AAAAAAA

FIGURE 16

```
</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436
<subunit 1 of 1, 300 aa, 1 stop
<MW: 32964, PI: 9.52, NX(S/T): 1
MKFLLDILLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAEGDVSILVNNAAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNGHIVTVASAAGHVSPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ
```

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

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FIGURE 17

FIGURE 18

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592
><subunit 1 of 1, 243 aa, 1 stop
><MW: 25298, pI: 6.44, NX(S/T): 0
MRPLLVLLLLGLAAGSPLLDDNKIPSLCPGHPGLPGTPGHGSQGLPGRDGRDGRDGAPGAP
GEKGEGRGPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP
FDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDFSGFLVYSDWHSSPVFA
```

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

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FIGURE 19

CTCTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCCTGGCGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG
GCACCACCTGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTCTTGCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA
GCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCAACTGGCTCAAG
CCAGGGCAGCCCTGTGGAATCCAACCCGAGCCTGGCATCCGGCTGTGGCGCACCTG
CAAGTGGCTGGAACATGCAGCTGCTGCCCGGGCTTGGCGTCCTTGTGAAGTGGTCAG
CCTATGGTTGCAGAGGGCAGCGGTACAGCCACGCCAGGAGAGTGTGCTCGAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGCCACCTCAAGCCAGCTGGCTGTGGCGGCAC
CTGTGCTCTGCAGGCCAGACAGCGATAAGCCTTGTCTGTGCCTACTCCCCGGAGGCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTCAAAGCCTGGGACCATGCAGGGGGCTCTGTGAGGTCCCC
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGGAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTC
ACGGCCGGTCCGGAGGAGGAGTGCTCGTGCCTGTGACATCGGCTACGGGGAGGCCAG
TGTGCCACCAAGGTGCATTTCCCTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAGGCG
GGGTGCTGGCCAGATCAAGAGCCAGAAAGTGCAAGGACATCCTCGCCTCTATCTGGCCGC
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTCTGGATCGGGCT
CACCTACAAGACGCCAAGGACTCCTCCGCTGGCCACAGGGGAGCACCAGGCCTCACCA
GTTTGCCTTGGCAGCCTGACAACCACGGCTGGTGTGGCTGAGTGCTGCCATGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTCACTGGAACGACCAGCGCTGAAAAC
CCGAAACCGTTACATCTGCCAGTTGCCAGGAGCACATCTCCGGTGGGCCAGGGTCC
GAGGCCTGACCACATGGCTCCCTGCCTGCCCTGGAGCACCGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCAGGTTAAGACCACATGCCTCATGTCAAAGAGGTCTCAGA
CCTTGCAACAATGCCAGAAGTTGGCAGAGAGAGGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG
AGTGTAGAAGAAGCTGGGCCCTCGCCTGCTTTGATTGGAAAGATGGCTCAATTAGA
TGGCGAAGGAGAGGACACCGCCAGTGGTCAAAAAGGCTGCTCTCCACCTGGCCAGAC
CCTGTGGGCAGCGGAGCTCCCTGTGGCATGAACCCACGGGTATTAAATTATGAATCAG
CTGAAAAAAAAAAAAA

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176
<subunit 1 of 1, 455 aa, 1 stop
<MW: 50478, pI: 8.44, NX(S/T): 2
MLHPETSPGRGHLLAVLLALLGTTWAEVWPQLQEQAPMAGALNRKESFLLSLHNRLRSWV
QPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWMQLLPAGLASFVEVV
SLWFAEGQRYSHAAGECARNATCTHYTQLWATSSSQLGCRHLCAGQTAIEAFVCAYSPGG
NWEVNGKTIIPYKKGAWSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSQNHGRLNISTCH
CHCPPGYTGRYCQVRCSLQCVHGRFREEECSVCDIGYGGAQCATKVHFPFHTCDLRIDGDC
FMVSSEADTYYRARMKCQRKGGLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIG
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWL SAAMGFNCVELQASAAFNWNDQRCK
TRNRYICQFAQEHI SRWGP GS

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442

FIGURE 21

CGGACGCGTGGCTGGCGCTGCAAAGCGTCCCCGGGTCCCCGAGCGTCCCCGCCCT
CGCCCCGCCATGCCTGCTGCTGGGCTGTGCCTGGGCTGTCCCTGTGTGGGGTCGCA
GGAAGAGGGCGCAGAGCTGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGAAG
TCAGACTGTTGAGGGCTGAAAACCAACCTTGATGACAGAATTCTCAGTGAAGTCTACC
ATCATTCCCCTATGCCTCACTACGGTTCTGCAGAATGCTAACAGAGCTCTGAAGA
CCAGGACATTGAGTTCCAGATGCAGATTCCAGCTGCAGCTTCATCACCAACTCACTATGC
TTATTGGAGACAAGGTGTATCAGGGCAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGG
GTAAAAGAGAAAAGGAATAAAACACAGAAGAAAATGGAGAGAAGGGGACTGAAATATTCA
AGCTTCTGCAGTGATTCCCAGCAAGGACAAAGCCGCTTTCTGAGTTATGAGGAGCTTC
TGCAGAGGCCTGGCAAGTACGAGCACAGCATCAGCGTGCAGCCAGCAGCTGTCCGG
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCCGATCGCATCCCTGGAGGTGCTGCC
GCTTCACAACAGCAGGCAGAGGGCAGTGGCGGGAGATGATTCTGGCCTCCCCAT
CTACTGTCTTAACCAAAATGAAACATTGCCAACATAATTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCAGAATGGAATTGGAGACTTATCATTAGATATGACGTCAATAG
AGAACAGAGCATTGGGACATCCAGGTTCTAAATGGCTATTGTGCACTACTTGCTCCTA
AAGACCTCCTCCTTACCAAGAATGTGGTATTGCTGACAGCAGTGCTTATGGTG
GGAACCAAACCTCCGGCAGACCAAGGATGCCCTTCACAATTCTCCATGACCTCCGACCCCA
GGACCGTTCACTGATTCCAGACAGCATCAGGGATGGGAAAGTGTACATTACCATATGTCACCCACTGGA
GGCACAGACATCAACGGGCCCTGCAGAGGGCATTAGGCTCCTCAACAAGTACGTGGCCA
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTCCTGACGGATGGAGGCCACGG
TCGGGGAGACGCACACCTCAAGATCCTCAACAAACACCCGAGAGGCCCGAGGGCAAGTC
TGCATCTCACCATTGGCATCGCAACGACGTGGACTTCAGGCTGCTGGAGAAACTGTCGCT
GGAGAACTGTGGCCTCACACGGCGTGCAGAGGGAGCGCAGGCTCGCAGCTCATCG
GGTTCTACGATGAAATCAGGACCCGCTCTCTGACATCCGCATCGATTATCCCCCAGC
TCAGTGGTGCAGGCCACCAAGACCCCTGTTCCCAACTACTTCAACGGCTGGAGATCATCAT
TGCAGGAAAGCTGGTGGACAGGAAGGCTGGATCACCTGCACGTGGAGGTACCGCAGCAACA
GTAAGAAATTCATCATTGAAAGACAGATGTGCTGTGCGGCCCTCAGAAGGCAGGGAAAGAT
GTCACAGGAAGCCCCAGGCCCTGGAGGCATGGAGAGGGGACACCAACCACATCGAGCGTCT
CTGGAGCTACCTCACCAAAAGGAGCTGCTGAGCTCTGGCTGCAAAGTGACGATGAACCGG
AGAAGGAGCGGCTGGCAGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCTCACTCCC
TTCACCTCCATGAAGCTGAGGGGGCGTCCACCGATGGATGGCCTGGAGGAGGCCACGG
CATGTCGGCTGCCATGGACCCGAACCGGGTGGCAGAGCGTGCAGGAGCTGGCACCGCAGC
CAGGACCTTGCTCAAGAAGCCAAACTCCGTCAAAAAAAACAAAACAAAACAAAAAAAGA
CATGGGAGAGATGGTGTGTTCTCCACCACTGGGGATACGATGAGAAGATGGCCACCT
GCAAGCCAGGAAGACGCCCTCACAGACACCAGTCTGCTGGCACCTGATCTGGACCTC
CCAGCCTCCAGAACTGTGAGAAATAATGTGTTAAGCTAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192
<subunit 1 of 1, 694 aa, 1 stop
<MW: 77400, pi: 9.54, NX(S/T): 6
MLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPQRVRLQLKTKPLMTEFSVKSTIIS
RYAFTTVSCRMLNRASEDQDIEFQMQIPAAAFITNFTMLIGDKVYQGEITEREKSGDRVKE
KRNKTTTENGEKGTEIFRASAVIPSVDKAFFLSYEELLQRRLGKYEHSISVRPQQQLSGRLS
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIIFKPTVVQQAR
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFVLDSSASMVGTK
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVWKDHLISVTPDSIRDGKVIHHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNNTREAARGQVCIF
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEIIIAGKLVDRKLDHLHVEVTASNNSKKFIILKTDVPVRPQKAGKDVTG
SPRPGGDGEGETNHIERLWSYLTtkellsswlQSDDEPEKERLRQRAQALAVSYRFLTPFTS
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKQNKTKRHGR
DGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

FIGURE 23

CGGACGCGTGGGTGCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC
GGCAGCGCGCGCGCGCCCTCCCGGGCTCCGGCTCTGCTGTTGCTCTTCTCCGCCCG
CACTGATCCCCACAGGTGATGGGCAGAATCTGTTACGAAAGACGTGACAGTGATCGAGGG
GAGGTTGCGACCATCAGTGCCAAGTCAATAAGAGTGACGACTCTGTGATTCAAGCTACTGAA
TCCCAACAGGCAGACCATTATTCAGGGACTTCAGGCCTTGAAGGACAGCAGGTTCACT
TGCTGAATTTCTAGCAGTGAACCAAAGTATCATTGACAAACGTCTCAATTCTGATGAA
GGAAGATACTTTGCCAGCTCTACCGATCCCCACAGGAAAGTTACACCACCATCACAGT
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG
AGATTGAAGTCAACTGCACTGCTATGCCAGCAAGCCAGCAGACTATCAGGTGGTCAAA
GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC
CAGTCAGCTGATGCTGAAGGTGACAAGGAGGACGATGGGTCCCAGTGATCTGCCAGGTGG
AGCACCCCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGCACATT CAGATGACTTATCCTCTACAAGGCTTAACCCGGAAAGGGACGCGCTTGA
GTTAACATGTGAAGCCATCGGAAGCCCCAGCCTGTGATGGTAACCTGGGTGAGAGTCGATG
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCAACCTGTTCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGAAAGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCACAACATATCCTCTCCCACAACAACCACCA
CCACCACCAACCACCAACCACCATCCTTACCATCATCACAGATTCCCAGCAGGTGAAGAAGGC
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTGGCGGTGGTGGTGGTGGTGGTGG
GCTGTGCTTGCATCATTCTGGGCGCTATTTGCCAGACATAAAGGTACATACTCACTC
ATGAAGCCAAGGAGCCGATGACGCAGCAGACGAGACACAGCTATAATCAATGCAGAAGGA
GGACAGAACAACTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCTTTGTGTTCAAT
GAGGTGTCCAAC TGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

DRAFT - NOT FOR CITATION

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pi: 4.93, NX(S/T): 7
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QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEETIEVNCTAMASKPATTIRWFKGNTTELKG
KSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT
YPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYR
CEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTILTIITDSRAGEEGSIRAVDH
AVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

FIGURE 25

GGGGCGGGTGGACCGGACTCGAACGCAGTTGCTCGGGACCCAGGACCCCCTGGGCCGA
CCCGCCAGGAAAGACTGAGGCCGCGCTGCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT
CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT
GGGGCCTGGGTGCAAGGCTGCCCATCCGGCTGCCAGTGAGCCACAGCACAGTCTTCT
GCACTGCCCGCAGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGCTGTAC
GTCTTGAGAACGGCATCACCATGCTGACGCAAGCAGCTTGCCGGCTGCCGGCTGCA
GCTCCTGGACCTGTACAGAACAGATGCCAGCCTGCCCTGCCCTGGAGCCGGCATCTGGACACTGCCAACGTGGAG
ACCTCAGCCACAACAGCCTCTGCCCTGGAGCCGGCATCTGGACACTGCCAACGTGGAG
GCGCTGCCGGCTGGCTGGCTGCCCTGCAGCAGCTGGACAGGGCTTCAAGCCGTTGCG
CAACCTCCACGACCTGGATGTGCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG
GCCCTCCGGGGCTGACGCCCTGCCCTGGCCGGCAACACCCGATTGCCAGCTGCCGCC
GAGGACCTGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAACGCTGCAGGC
CCTGCCCTGGCAGCTCTGCCCTCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCAACC
CCTTCAACTGCGTGTGCCCTGAGCTGGTTGCCCTGGGTGCCGAGAGGCCACGTACA
CTGCCAGCCCTGAGGAGACGCCCTGCCACTGCCCAAGAACGCTGCCGGCTGCTCCT
GGAGCTTGACTACGCCACTTGGCTGCCAGGCCACCACAGGCCACAGTGCACCA
CGAGGCCGTGGTGCAGGGAGCCACAGCCTGTCTTAGCTTGCTCCTACCTGGCTTAGC
CCCACAGGCCGGCACTGAGGCCAGGCCAGGCCCTCCACTGCCCAAGGACTGTAGGGCC
TGTCCCCCAGGCCAGGACTGCCACCGTCCACCTGCCCTAACGGGGCACATGCCACCTGG
GGACACGGCACCACCTGGCGTGTGCCCGAAGGCTTCAGGGCTGTACTGTGAGAGC
CAGATGGGGCAGGGACACGCCAGCCCTACACCAGTCAGGCCAGGCCACACGGTCCCT
GACCTGGGATCGAGGCCGGTGAAGGCCACCTCCCTGCCGTGGGCTGCCAGCTACCTCC
AGGGGAGCTCCGTGAGCTCAGGAGCCTCCGTCTCACCTATGCCAACCTATGCCCTGAT
AAGCGGCTGGTACGCTGCACTGCCCTGCCCTGCCCTGAGTACACGGTCAACAGCTGCC
GCCCAACGCCACTTACTCCGTCTGTGTCATGCCCTGGGGCCGGGGTGCCGGAGGGCC
AGGAGGCTGCCGGGAGGCCATACACCCCAAGCCGTCCACTCCAACCACGCCAGTCACC
CAGGCCCGCAGGGCAACCTGCCCTCATTGCCCGCCCTGCCGGGTGCTCCTGGC
CGCGCTGGCTGCCGTGGGCAAGCCTACTGTGTGCCGGGGGGCCATGGCAGCAGCGG
CTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGGCCACTGGGACTGGAGAGGCCCTGCC
GTGTGAGGTGCCACTCATGGGCTCCAGGGCTGCCAGTCAACCCCTCACGCCAAAGC
CCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAGATGGC
CAGCCCCCTCTGCCACACCACGTAAGTCTCAGTCCAAACCTGCCGGATGTGCAAGA
CAGGGCTGTGACCAACAGCTGGCCCTGTTCCCTCTGCCACCTGCCGTCTCCTCATCTGTGAG
ATGCTGTGCCAGCTGACGAGCCCTAACGTCAGTCCCCAGAACCGAGTGCTATGAGGACAGTGT
CCGCCCTGCCCTCCGCAACGTGCAGTCAGTCCCTGCCAGGGCAGGCCCTGCCATGTGCTGGTAAC
GCATGCCCTGGGCCCTGCTGGCTCTCCACTCCAGGCCACCTGCCGGGGCCAGTGAAGGAAG
CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCCGTGTGACTCTAGTCTTGGGCCAGG
AAGCGAAGGAACAAAAGAAACTGGAAAGGAAGATGCTTAGGAACATGTTGCTTTAA
AATATATATATTTATAAGAGATCCTTCCCATTATTCTGGGAAGATGTTTCAAAC
AGAGACAAGGACTTGGTTTGTAAAGACAAACGATGATGATGAAGGCCTTGTAAAGAAAAA
ATAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pi: 7.24, NX(S/T): 3

MCSRVPLLLPLLLLALGPGVQGCPSCQCQPQTVFCTARQGTTVPRDVPPDTVGLYVFEN
GITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVEALRL
AGLGLQQQLDEGLFSRLRNLDLVDSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA
GLAALQELDVSNLSQLPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRESHVTLASP
EETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSLAPTWLSPTAP
ATEAPSPPSTAPPTVGVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQ
GTRPSPTPVTPRPPRSLTIGIEPVSPSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLV
TLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEAACGEAHTPPAVHSNHAPVTQARE
GNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAQDKGQVGPGAGPLELEGVKVPLEP
GPKATEGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

FIGURE 27

GGCACTAGGACAAACCTTCTTCCCTCTGCACCACTGCCGTACCCCTACCGCCCCGCCACC
TCCTTGCTACCCCACTCTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTCATGCCAGCCTC
ATCTCCTTCTGCTAGCCCCAAAGGGCCTCCAGGCAACATGGGGGCCAGTCAGAGAGC
CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGCAGCTCTGGGGCCGTGGCTTGCC
ATGGCTCTGCTGACCCAAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
GGGGACAGGAGGCCCCCTCCCAGAATGGGAAGGGTATCCCTGGCAGAGTCTCCGGAGCAGA
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC
ACCCAAAAACAGAAGAAGCAGCACTCTGCTCTGCACCTGGTCCCATTACGCCACCTCCAA
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTAGGCGTGGAGAGGCCTAC
AGGCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTATCTGCTGTAGGCCAGGTC
CTGTTCAAGACGTGACTTCACCATGGTCAGGTGGTCTCGAGAAGGCCAAGGAAGGCA
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGGACCGGCCTACAACAGCT
GCTATAGCGCAGGTGTCTTCCATTACACCAAGGGATATTCTGAGTGTCTAATTCCCCGG
GCAAGGGCGAAACTTAACCTCTCCACATGGAACCTTCTGGGTTGTGAAACTGTGATT
GTGTTATAAAAAGTGGCTCCAGCTTGGAAAGACCAGGGTGGTACATACTGGAGACAGCCAA
GAGCTGAGTATATAAGGAGAGGAATGTGCAGGAACAGAGGCATCTTCTGGGTTGGCTC
CCCGTTCCACTTTCCCTTCAATTCCCACCCCTAGACTTGTGATTACGGATATCTTGC
CTTCTGTTCCCCATGGAGCTCCG

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, PI: 9.85, NX(S/T): 2

MPASSPFL LAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV
SRLQGTGGPSQN GEGYPWQLPEQSSDALEAWENGERSRKRRAVLTQKQKKQHSV LHLVPIN
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVR IQDAGVYLLYSQVLFQDVFTMGQVV SREG
QGRQETLFRCIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA KLNLSPHGTFLGFVKL

Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

FIGURE 29

CACTTCTCCCTCTTCTTACTTCGAGAAACCGCGCTCCGCTTGGTCGCAGAGAC
CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTGGGTGGGGGACCTGTGGCTGCTCGTA
CCGCCCCCCCACCCTCCTCTGCAGTGCCTCCGGAACCTGGCGGGAGGAGGCTTGGCCGGCGGGAGA
TCCTCACCGAGTCTGTGCATGCCCGGACCTGGCGGGAGGAGCAGGAGGGCCGGCAGGAAGATGGGC
TCCCCTGGACAGGGACTCTGCTGGCGTACTGCCTGCTCCTGCCTTGCCCTGGCCTGGT
CCTGAGTCGTGTGCCCATGTCCAGGGGAACAGCAGGAGTGGGAGGGACTGAGGAGCTGC
CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACACATGAAAATACAGGCCAGTCAG
GACCAGGGCTCCCTGCTTCCGGTCTCGCTGCTGTGACCCGGTACCTCCATGTACCC
GGCAGCCGTGCCAGATCAACATCACTATCTGAAAGGGAGAAGGGTACCGCCGGAG
ATCGAGGCCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGCCAGGGCCACACTGGA
CCAAAGGGAGAAGGGCTCCATGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
CTTTCTGGTGGGCCGGAGAAGCCCAGTGCACAGCAACACTACTACCAAGACGGTATCTCG
ACACGGAGTCGTGAACCTCTACGACCACTCAACATGTTCACCGGCAAGTTCTACTGCTAC
GTGCCCGCCTCTACTTCTCAGCCTCAACGTGCACACCTGGAACCAGAAGGAGACCTACCT
GCACATCATGAAGAACGAGGAGGTGGTATCTTCTCGCGCAGGTGGCGACCGCAGCA
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCGAGGTGGTACGCC
TACAAGGGCGAACGTGAGAACGCCATCTCAGCGAGGAGCTGGACACCTACATCACCTCAG
TGGCTACCTGGTCAAGCACGCCACCGAGCCTAGCTGGCCGGCCACCTCCTCTCGCC
ACCTTCCACCCCTCGCTGTGCTGACCCCACCGCCTCTCCCGATCCCTGGACTCCGACTC
CCTGGCTTGGCATTCACTGAGACGCCCTGCACACACAGAAAGCAAAGCGATCGGTGCTCC
CAGATCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAAGGGCGGGCACCCGC
GAGAACCCCTGGGACCTTCCGGCCCTCTGCACACATCCTCAAGTGACCCGCACGGC
GAGACGGGTGGCGCAGGGCGTCCCAGGGTGC GG CACCGCGGCTCCAGTCTGGAAATA
ATTAGGCAAATTCTAAAGGTCTAAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG
TTGTTATTTGTCTTCCAGCCAGCCTGCTGGCTCCAAAGAGAGAGGGCTTTCAGTTGAG
ACTCTGCTTAAGAGAACATCCAAAGTTAAAGCTCTGGGTCAAGGGAGGGCCGGGCAGG
AAACTACCTCTGGCTTAATTCTTTAAGCCACGTAGGAACCTTCTTGAGGGATAGGTGGACC
CTGACATCCCTGTGGCCTTGCACAGGGCTCTGCTGGTCTTCTGAGTCACAGCTGCGAGGT
GATGGGGCTGGGCCAGGGCTCAGCCTCCAGAGGACAGCTGAGCCCCCTGCCTGGC
TCCAGGGTGGTAGAACGAGCCGAAGGGCTCCTGACAGTGGCCAGGGACCCCTGGTCCCCA
GGCCTGCAGATGTTCTATGAGGGCAGAGCTCCTGGTACATCCATGTGTGGCTCTGCTCC
ACCCCTGTGCCACCCAGAGCCCTGGGGGTGGTCTCCATGCCTGCCACCTGGCATCGGCT
TTCTGTGCCGCCCTCCCACACAAATCAGCCCCAGAAGGCCCGGGCTTGGCTCTGTTTT
TATAAAACACCTCAAGCAGCACTGCAGTCTCCATCTCCTCGTGGCTAACGATCACCGCTT
CCACGTGTGTTGGTGGCAGCAAGGCTGATCCAGACCCCTCTGCCCTGGGACTGCG
CATCCAGGCCTCTGACCAAGTAGCCTGAGAGGGCTTTCTAGGCTTCAGAGCAGGGAGAG
CTGGAGGGCTAGAAAGCTCCGCTGTCTGTTCTCAGGCTCCTGTGAGGCTCAGCCTG
AGACCAGAGTCAGAGGAAGTACACGTCCAATCACCGTGTCAAGGATTCACTCTCAGGAGC
TGGGTGGCAGGAGAGGAATAGCCCCTGTGGCAATTGCAGGACAGCTGGAGCAGGGTTGCG
GTGTCTCCACGGTGCCTCGCCCTGCCATGCCACCCAGACTCTGATCTCCAGGAACCC
ATAGCCCCTCTCCACCTCACCCATGTTGATGCCAGGGTCACTCTGCTACCCGCTGGGCC
CCCAAACCCCCGCTGCCCTCTTCCCTCCCCCATCCCCCACCTGGTTTGACTAATCCTGC
TTCCTCTCTGGGCTGGCTGCCGGATCTGGGCTCCCTAAGTCCCTCTCTTAAAGAACTT
CTGCGGGCTAGACTCTGAAGCCGAGTTGCTGTGGCGTGCCCGGAAGCAGAGGCCACACTC
GCTGCTTAAGCTCCCCAGCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTCAA

FIGURE 30

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSGRKPKMHSNHYYQTVIFDTEFVNLYDHFNMF TGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEVVILFAQVGDRSIMQSQSLMELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP
```

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 31

GGGGAGCATCCGCTCGGGCCTCGCCGAGACCCCCGCGCGGATTGCCGGTCCTCCCGCGG
GCGCGACAGAGCTGCCTCGCACCTGGATGGCAGCAGGGCGCCGGGTCTCTCGACGCCA
GAGAGAAATCTCATCATCTGTGCAGCCTTAAAGCAAACATAAGACCAAGAGGAGGATTAT
CCTTGACCTTGAGAACAAAACACTAAACTGAAATTAAAATGTTCTCGGGGAGAAGGGAG
CTTGACTTACACTTGTAATAATTGCTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTCTAAGGGAATC
AGAGGCAATGAGCCCCTATATACTTCAACTCAAGAAGACTGCATTAATTCTGCTGTTAAC
AAAAAACATATCAGGGACAAAGCATGTAATTGATGATCTCGACACTCGAAAAACAGCTA
GACAACCCAAC TGCTACCTATTTCTGCTCCAACGAGGAAGCCTGTCATTGAAACCAGCA
AAAGGACTTATGAGTTACAGGATAATTACAGATTTCATCTTGACCAGAAATTGCCAAG
CCAAGAGTTACCCCAGGAAGATTCTCTCTACATGCCAATTTCACAAGCAGTCACCTCCC
TAGCCCACATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT
CAGAAGTTGGATCCTCAGATCACCTGGAGAAACTATTAAGATGGATGAAGCAAGTCCCCA
GCTCCTGCTTATAAGGAAAAGGCCATTCTCAGAGTTACAATTTCCTCTGATCAAGAAA
TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA
CATACCACCTCGGCTACTCCAAAGCCGCCACCTCTACCCACCAATGCTCAGTGACACC
TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACCTCTC
AGCCTCCCACGACCCCTCATTTCTACAGTTTACACGGGCTGCGGCTACACTCCAAGCAATG
GCTACAACAGCAGTCTGACTACCACCTTCAGGCACCTACGGACTCGAAAGGCAGCTAGA
AACCATACCAGTTACAGAAATCTCAAACTTAACATTGAACACAGGAATGTGTATAACCTA
CTGCACTTCTATGTCAGGAAATGTGGAGTCTCCACTATGAATAAAACTGCTCCTGGGAAGGT
AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTTCAGAAAATCAGTACGGCCTTCC
ATTGAAAATGGCTTCTATGGGTCCCTGCTTTGGTGTCTGGTGTACTCAAGACTGGAT
TCGTCTCCTGGTAGAATCCTTCGGAATCACTCCGCAAGGAAACGTTACTCAAGACTGGAT
TATTGATCAATGGATCTATGTGGACATCTAAAGGATGGAACACTGGTGTCTTAATTCTT
TAGTAACCAGAAGCCAAATGCAATGAGTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
TATTGAAAGACAGGAAATGCCCTCTGCTTTCTGGTGTCTGGGAGACAGAGTCTT
GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTGGCTCTCACCGAACCTCCGTCTC
CTGGGTTCAAGCGATTCTCCTGCCCTAGCCTCTAAGTATCTGGATTACAGGCATGTGCCA
CCACACCTGGGTGATTTGTATTTAGTAGAGACGGGTTTACCATGTTGGTCAGGCTG
GTCTCAAACCTGACCTAGTGTGATCCACCCCTCGGCCTCCAAAGTGCTGGATTACAGG
CATGAGCCACACAGCTGGCCCCCTCTGTTTATGTTGGTTTGAGAAGGAATGAAGTG
GGAACCAAATTAGGTAAATTGGTAATCTGCTCTAAATATTAGCTAAAACAAAGCTCT
ATGTAAGTAATAAGTATAATTGCCATATAAATTCAAACGGCTTTATGCAA
GAAACAGGTTAGGACATCTAGGTTCCAATTCACATTCTGGTCCAGATAAAATCAAC
TGTTTATATCAATTCTAATGGATTGCTTTCTTTATGGATTCCCTTAAACTTATT
CCAGATGTAGTTCCATTAAATATTGAATAATCTTTGTTACTCAA

FIGURE 32

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVIICFLRLSASQNCLKKSLEDVVIDIQSSLKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPPTLISTVFTRAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTLNNTGNVYNPTALSMSNVESSTMNKTAWEGRREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 33

GC GG CAC CT GG AAG **A**T GCG CCC ATT GG CT GG TGG C CT GCT CA AGG TGG TGT CGT GGG CT TC
GC CT CTT GT GT GC CT GG TATT CGGG GT AC CT GCT CG CAG AG CT CATT CC AG AT GC ACCC CT
GT CC AG TG CT GC CT AT AG CAT CCC CAG CAT CGGG AG AGG CCT GT CCT CAA AG CT CC AGT CC
CC AAA AGG CAAA AT GT GACC ACT GG ACT CC CT GCCC AT CT GAC ACCT AT GC CT AC AGG TT A
CT CAG CGG AGG GT GG CAG AAG CA AGT AC G C CAAA AT CT GCT TT GAGG ATA ACCT ACT TAT GGG
AGA AAC AGC TGG AA AT GTT GCC AGAGGA AT AA AC ATT GCC ATT GT CA ACT AT GT AACT GGG A
AT GT GAC AG CA AC AC GAT GT TT GAT AT GT AT GA AGG CG AT A ACT CT GG ACC CG AT GACA AAG
TTT ATT CAG AGT GCT GCT CAAA AT CC CT GCT CTT CAT GGT GAC CT AT GAC GAC GGA AGC AC
AAG ACT GA AT AAC GAT GCCA AGA AT GCC AT AGA AGC ACT TGG AAGT AA AGA AA AT CAGG AACA
TG AA ATT CAG GT CT AG CT GGG TATT ATT GCAG CAAA AGG CTT GG AACT CC CT CC GAA ATT
CAG AG AG AAA AG AT CA ACC ACT CT GAT GCT AAG AACA AC AG AT ATT CT GG CT GG CCT GC AGA
GAT CC AGA T AGA AGG CT GC AT ACC CAA AGA AC AGC **TG A** CACT GCAG GG CCT GAG TAA AT
GT GT T CT GT AT AA ACA AA AT GCAG CT GG AAT CG CT CA AGA AT CTT ATT TT CT AA AT CCA ACA
GCC CAT ATT GAT GAG T ATT TGG TT GT AA ACCA AT GA AC ATT GCT AG TT GT AT CA
AAT CTT GGT AC G CAG T ATT TT AT ACC AGT ATT T AT GT TAG TGA AG AT GT CA ATT AG CAG GA
AACT AAA AT GA AT GG AA ATT CT T AAAA AAAAAA A

FIGURE 34

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777
><subunit 1 of 1, 235 aa, 1 stop
><MW: 25982, pI: 9.09, NX(S/T): 2
MRPLAGGLLKVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMDYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS
```

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125